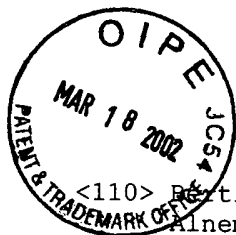


45



SEQUENCE LISTING

<110> Reitin, John
Alnemri, Emad S.

<120> NOVEL MOLECULES OF THE CARD-RELATED
PROTEIN FAMILY AND USES THEREOF

<130> 07334-335001

<140> 09/931,071

<141> 2001-08-15

<150> 09/428,252

<151> 1999-10-27

<160> 11

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 5444

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (523)...(4809)

<400> 1

```

gccccagggc ctggagaggt ctgaagaaac ctgggagcca gcagcccggg gctccactct      60
gggttctgaa agcccattcc ctgctctgcg gctcctccca cccacacctt tctcagcctt      120
gcagctcaag ggttgatctc aggagtccag gacccaggag agggaagaat ctgaggaaca      180
cagaacagtg agcgttgccc acaccccatc tcccgtcacc acatctcccc tcaccctcac      240
cctccctgcc tggccctgga ccccatccca ggacctccct atcagctgac ttcttccagt      300
gtcttgaggg cccctctggg ctctctccct cctgggcttt tcttaccact cccctcttat      360
cggcgtctat ctgtagggtgc cctgggattt ataaaactgg gttccgaatg ctgaataaga      420
gacggtaaga gccaaaggcaa aggacagcac tgttctctgc ctgcctgata ccctcaccac      480
ctgggaacat cccccagaca cctctttaac tccgggacag ag atg gct ggc gga      534

```

Met Ala Gly Gly

1

```

gcc tgg ggc cgc ctg gcc tgt tac ttg gag ttc ctg aag aag gag gag      582
Ala Trp Gly Arg Leu Ala Cys Tyr Leu Glu Phe Leu Lys Lys Glu Glu
  5              10              15              20

```

```

ctg aag gag ttc cag ctt ctg ctc gcc aat aaa gcg cac tcc agg agc      630
Leu Lys Glu Phe Gln Leu Leu Leu Ala Asn Lys Ala His Ser Arg Ser
      25              30              35

```

```

tct tcg ggt gag aca ccc gct cag cca gag aag acg agt ggc atg gag      678
Ser Ser Gly Glu Thr Pro Ala Gln Pro Glu Lys Thr Ser Gly Met Glu
      40              45              50

```

```

gtg gcc tcg tac ctg gtg gct cag tat ggg gag cag cgg gcc tgg gac      726

```

Val	Ala	Ser	Tyr	Leu	Val	Ala	Gln	Tyr	Gly	Glu	Gln	Arg	Ala	Trp	Asp	
	55						60					65				
cta	gcc	ctc	cat	acc	tgg	gag	cag	atg	ggg	ctg	agg	tca	ctg	tgc	gcc	774
Leu	Ala	Leu	His	Thr	Trp	Glu	Gln	Met	Gly	Leu	Arg	Ser	Leu	Cys	Ala	
	70					75					80					
caa	gcc	cag	gaa	ggg	gca	ggc	cac	tct	ccc	tca	ttc	ccc	tac	agc	cca	822
Gln	Ala	Gln	Glu	Gly	Ala	Gly	His	Ser	Pro	Ser	Phe	Pro	Tyr	Ser	Pro	
	85				90					95					100	
agt	gaa	ccc	cac	ctg	ggg	tct	ccc	agc	caa	ccc	acc	tcc	acc	gca	gtg	870
Ser	Glu	Pro	His	Leu	Gly	Ser	Pro	Ser	Gln	Pro	Thr	Ser	Thr	Ala	Val	
				105					110					115		
cta	atg	ccc	tgg	atc	cat	gaa	ttg	ccg	gcg	ggg	tgc	acc	cag	ggc	tca	918
Leu	Met	Pro	Trp	Ile	His	Glu	Leu	Pro	Ala	Gly	Cys	Thr	Gln	Gly	Ser	
			120					125					130			
gag	aga	agg	gtt	ttg	aga	cag	ctg	cct	gac	aca	tct	gga	cgc	cgc	tgg	966
Glu	Arg	Arg	Val	Leu	Arg	Gln	Leu	Pro	Asp	Thr	Ser	Gly	Arg	Arg	Trp	
		135					140					145				
aga	gaa	atc	tct	gcc	tca	ctc	ctc	tac	caa	gct	ctt	cca	agc	tcc	cca	1014
Arg	Glu	Ile	Ser	Ala	Ser	Leu	Leu	Tyr	Gln	Ala	Leu	Pro	Ser	Ser	Pro	
	150					155					160					
gac	cat	gag	tct	cca	agc	cag	gag	tca	ccc	aac	gcc	ccc	aca	tcc	aca	1062
Asp	His	Glu	Ser	Pro	Ser	Gln	Glu	Ser	Pro	Asn	Ala	Pro	Thr	Ser	Thr	
	165					170				175					180	
gca	gtg	ctg	ggg	agc	tgg	gga	tcc	cca	cct	cag	ccc	agc	cta	gca	ccc	1110
Ala	Val	Leu	Gly	Ser	Trp	Gly	Ser	Pro	Pro	Gln	Pro	Ser	Leu	Ala	Pro	
			185						190						195	
aga	gag	cag	gag	gct	cct	ggg	acc	caa	tgg	cct	ctg	gat	gaa	acg	tca	1158
Arg	Glu	Gln	Glu	Ala	Pro	Gly	Thr	Gln	Trp	Pro	Leu	Asp	Glu	Thr	Ser	
		200						205					210			
gga	att	tac	tac	aca	gaa	atc	aga	gaa	aga	gag	aga	gag	aaa	tca	gag	1206
Gly	Ile	Tyr	Tyr	Thr	Glu	Ile	Arg	Glu	Arg	Glu	Arg	Glu	Lys	Ser	Glu	
	215						220					225				
aaa	ggc	agg	ccc	cca	tgg	gca	gcg	gtg	gta	gga	acg	ccc	cca	cag	gcg	1254
Lys	Gly	Arg	Pro	Pro	Trp	Ala	Ala	Val	Val	Gly	Thr	Pro	Pro	Gln	Ala	
	230					235					240					
cac	acc	agc	cta	cag	ccc	cac	cac	cac	cca	tgg	gag	cct	tct	gtg	aga	1302
His	Thr	Ser	Leu	Gln	Pro	His	His	His	Pro	Trp	Glu	Pro	Ser	Val	Arg	
	245				250					255					260	
gag	agc	ctc	tgt	tcc	aca	tgg	ccc	tgg	aaa	aat	gag	gat	ttt	aac	caa	1350
Glu	Ser	Leu	Cys	Ser	Thr	Trp	Pro	Trp	Lys	Asn	Glu	Asp	Phe	Asn	Gln	
			265					270						275		
aaa	ttc	aca	cag	ctg	cta	ctt	cta	caa	aga	cct	cac	ccc	aga	agc	caa	1398
Lys	Phe	Thr	Gln	Leu	Leu	Leu	Leu	Gln	Arg	Pro	His	Pro	Arg	Ser	Gln	

280	285	290	
gat ccc ctg gtc aag aga agc tgg cct gat tat gtg gag gag aat cga Asp Pro Leu Val Lys Arg Ser Trp Pro Asp Tyr Val Glu Glu Asn Arg 295 300 305			1446
gga cat tta att gag atc aga gac tta ttt ggc cca ggc ctg gat acc Gly His Leu Ile Glu Ile Arg Asp Leu Phe Gly Pro Gly Leu Asp Thr 310 315 320			1494
caa gaa cct cgc ata gtc ata ctg cag ggg gct gct gga att ggg aag Gln Glu Pro Arg Ile Val Ile Leu Gln Gly Ala Ala Gly Ile Gly Lys 325 330 335 340			1542
tca aca ctg gcc agg cag gtg aag gaa gcc tgg ggg aga ggc cag ctg Ser Thr Leu Ala Arg Gln Val Lys Glu Ala Trp Gly Arg Gly Gln Leu 345 350 355			1590
tat ggg gac cgc ttc cag cat gtc ttc tac ttc agc tgc aga gag ctg Tyr Gly Asp Arg Phe Gln His Val Phe Tyr Phe Ser Cys Arg Glu Leu 360 365 370			1638
gcc cag tcc aag gtg gtg agt ctc gct gag ctc atc gga aaa gat ggg Ala Gln Ser Lys Val Val Ser Leu Ala Glu Leu Ile Gly Lys Asp Gly 375 380 385			1686
aca gcc act ccg gct ccc att aga cag atc ctg tct agg cca gag cgg Thr Ala Thr Pro Ala Pro Ile Arg Gln Ile Leu Ser Arg Pro Glu Arg 390 395 400			1734
ctg ctc ttc atc ctc gat ggt gta gat gag cca gga tgg gtc ttg cag Leu Leu Phe Ile Leu Asp Gly Val Asp Glu Pro Gly Trp Val Leu Gln 405 410 415 420			1782
gag ccg agt tct gag ctc tgt ctg cac tgg agc cag cca cag ccg gcg Glu Pro Ser Ser Glu Leu Cys Leu His Trp Ser Gln Pro Gln Pro Ala 425 430 435			1830
gat gca ctg ctg ggc agt ttg ctg ggg aaa act ata ctt ccc gag gca Asp Ala Leu Leu Gly Ser Leu Leu Gly Lys Thr Ile Leu Pro Glu Ala 440 445 450			1878
tcc ttc ctg atc acg gct cgg acc aca gct ctg cag aac ctc att cct Ser Phe Leu Ile Thr Ala Arg Thr Thr Ala Leu Gln Asn Leu Ile Pro 455 460 465			1926
tct ttg gag cag gca cgt tgg gta gag gtc ctg ggg ttc tct gag tcc Ser Leu Glu Gln Ala Arg Trp Val Glu Val Leu Gly Phe Ser Glu Ser 470 475 480			1974
agc agg aag gaa tat ttc tac aga tat ttc aca gat gaa agg caa gca Ser Arg Lys Glu Tyr Phe Tyr Arg Tyr Phe Thr Asp Glu Arg Gln Ala 485 490 495 500			2022
att aga gcc ttt agg ttg gtc aaa tca aac aaa gag ctc tgg gcc ctg Ile Arg Ala Phe Arg Leu Val Lys Ser Asn Lys Glu Leu Trp Ala Leu 505 510 515			2070

tgt ctt gtg ccc tgg gtg tcc tgg ctg gcc tgc act tgc ctg atg cag Cys Leu Val Pro Trp Val Ser Trp Leu Ala Cys Thr Cys Leu Met Gln 520 525 530	2118
cag atg aag cgg aag gaa aaa ctc aca ctg act tcc aag acc acc aca Gln Met Lys Arg Lys Glu Lys Leu Thr Leu Thr Ser Lys Thr Thr Thr 535 540 545	2166
acc ctc tgt cta cat tac ctt gcc cag gct ctc caa gct cag cca ttg Thr Leu Cys Leu His Tyr Leu Ala Gln Ala Leu Gln Ala Gln Pro Leu 550 555 560	2214
gga ccc cag ctc aga gac ctc tgc tct ctg gct gct gag ggc atc tgg Gly Pro Gln Leu Arg Asp Leu Cys Ser Leu Ala Ala Glu Gly Ile Trp 565 570 575 580	2262
caa aaa aag acc ctt ttc agt cca gat gac ctc agg aag cat ggg tta Gln Lys Lys Thr Leu Phe Ser Pro Asp Asp Leu Arg Lys His Gly Leu 585 590 595	2310
gat ggg gcc atc atc tcc acc ttc ttg aag atg ggt att ctt caa gag Asp Gly Ala Ile Ile Ser Thr Phe Leu Lys Met Gly Ile Leu Gln Glu 600 605 610	2358
cac ccc atc cct ctg agc tac agc ttc att cac ctc tgt ttc caa gag His Pro Ile Pro Leu Ser Tyr Ser Phe Ile His Leu Cys Phe Gln Glu 615 620 625	2406
ttc ttt gca gca atg tcc tat gtc ttg gag gat gag aag ggg aga ggt Phe Phe Ala Ala Met Ser Tyr Val Leu Glu Asp Glu Lys Gly Arg Gly 630 635 640	2454
aaa cat tct aat tgc atc ata gat ttg gaa aag acg cta gaa gca tat Lys His Ser Asn Cys Ile Ile Asp Leu Glu Lys Thr Leu Glu Ala Tyr 645 650 655 660	2502
gga ata cat ggc ctg ttt ggg gca tca acc aca cgt ttc cta ttg ggc Gly Ile His Gly Leu Phe Gly Ala Ser Thr Thr Arg Phe Leu Leu Gly 665 670 675	2550
ctg tta agt gat gag ggg gag aga gag atg gag aac atc ttt cac tgc Leu Leu Ser Asp Glu Gly Glu Arg Glu Met Glu Asn Ile Phe His Cys 680 685 690	2598
cgg ctg tct cag ggg agg aac ctg atg cag tgg gtc ccg tcc ctg cag Arg Leu Ser Gln Gly Arg Asn Leu Met Gln Trp Val Pro Ser Leu Gln 695 700 705	2646
ctg ctg ctg cag cca cac tct ctg gag tcc ctc cac tgc ttg tac gag Leu Leu Leu Gln Pro His Ser Leu Glu Ser Leu His Cys Leu Tyr Glu 710 715 720	2694
act cgg aac aaa acg ttc ctg aca caa gtg atg gcc cat ttc gaa gaa Thr Arg Asn Lys Thr Phe Leu Thr Gln Val Met Ala His Phe Glu Glu 725 730 735 740	2742

atg ggc atg tgt gta gaa aca gac atg gag ctc tta gtg tgc act ttc Met Gly Met Cys Val Glu Thr Asp Met Glu Leu Leu Val Cys Thr Phe 745 750 755	2790
tgc att aaa ttc agc cgc cac gtg aag aag ctt cag ctg att gag ggc Cys Ile Lys Phe Ser Arg His Val Lys Lys Leu Gln Leu Ile Glu Gly 760 765 770	2838
agg cag cac aga tca aca tgg agc ccc acc atg gta gtc ctg ttc agg Arg Gln His Arg Ser Thr Trp Ser Pro Thr Met Val Val Leu Phe Arg 775 780 785	2886
tgg gtc cca gtc aca gat gcc tat tgg cag att ctc ttc tcc gtc ctc Trp Val Pro Val Thr Asp Ala Tyr Trp Gln Ile Leu Phe Ser Val Leu 790 795 800	2934
aag gtc acc aga aac ctg aag gag ctg gac cta agt gga aac tcg ctg Lys Val Thr Arg Asn Leu Lys Glu Leu Asp Leu Ser Gly Asn Ser Leu 805 810 815 820	2982
agc cac tct gca gtg aag agt ctt tgt aag acc ctg aga cgc cct cgc Ser His Ser Ala Val Lys Ser Leu Cys Lys Thr Leu Arg Arg Pro Arg 825 830 835	3030
tgc ctc ctg gag acc ctg cgg ttg gct ggc tgt ggc ctc aca gct gag Cys Leu Leu Glu Thr Leu Arg Leu Ala Gly Cys Gly Leu Thr Ala Glu 840 845 850	3078
gac tgc aag gac ctt gcc ttt ggg ctg aga gcc aac cag acc ctg acc Asp Cys Lys Asp Leu Ala Phe Gly Leu Arg Ala Asn Gln Thr Leu Thr 855 860 865	3126
gag ctg gac ctg agc ttc aat gtg ctc acg gat gct gga gcc aaa cac Glu Leu Asp Leu Ser Phe Asn Val Leu Thr Asp Ala Gly Ala Lys His 870 875 880	3174
ctt tgc cag aga ctg aga cag ccg agc tgc aag cta cag cga ctg cag Leu Cys Gln Arg Leu Arg Gln Pro Ser Cys Lys Leu Gln Arg Leu Gln 885 890 895 900	3222
ctg gtc agc tgt ggc ctc acg tct gac tgc tgc cag gac ctg gcc tct Leu Val Ser Cys Gly Leu Thr Ser Asp Cys Cys Gln Asp Leu Ala Ser 905 910 915	3270
gtg ctt agt gcc agc ccc agc ctg aag gag cta gac ctg cag cag aac Val Leu Ser Ala Ser Pro Ser Leu Lys Glu Leu Asp Leu Gln Gln Asn 920 925 930	3318
aac ctg gat gac gtt ggc gtg cga ctg ctc tgt gag ggg ctc agg cat Asn Leu Asp Asp Val Gly Val Arg Leu Leu Cys Glu Gly Leu Arg His 935 940 945	3366
cct gcc tgc aaa ctc ata cgc ctg ggg ctg gac cag aca act ctg agt Pro Ala Cys Lys Leu Ile Arg Leu Gly Leu Asp Gln Thr Thr Leu Ser 950 955 960	3414
gat gag atg agg cag gaa ctg agg gcc ctg gag cag gag aaa cct cag	3462

1190	1195	1200	
ata gtt ctg gaa aac ccc agc ttc tcc ccc ttg gga gtc ctc ctg aaa Ile Val Leu Glu Asn Pro Ser Phe Ser Pro Leu Gly Val Leu Leu Lys 1205 1210 1215 1220			4182
atg atc cat aat gcc ctg cgc ttc att ccc gtc acc tct gtg gtg ttg Met Ile His Asn Ala Leu Arg Phe Ile Pro Val Thr Ser Val Val Leu 1225 1230 1235			4230
ctt tac cac cgc gtc cat cct gag gaa gtc acc ttc cac ctc tac ctg Leu Tyr His Arg Val His Pro Glu Glu Val Thr Phe His Leu Tyr Leu 1240 1245 1250			4278
atc cca agt gac tgc tcc att cgg aag gaa ctg gag ctc tgc tat cga Ile Pro Ser Asp Cys Ser Ile Arg Lys Glu Leu Glu Leu Cys Tyr Arg 1255 1260 1265			4326
agc cct gga gaa gac cag ctg ttc tcg gag ttc tac gtt ggc cac ttg Ser Pro Gly Glu Asp Gln Leu Phe Ser Glu Phe Tyr Val Gly His Leu 1270 1275 1280			4374
gga tca ggg atc agg ctg caa gtg aaa gac aag aaa gat gag act ctg Gly Ser Gly Ile Arg Leu Gln Val Lys Asp Lys Lys Asp Glu Thr Leu 1285 1290 1295 1300			4422
gtg tgg gag gcc ttg gtg aaa cca gga gat ctc atg cct gca act act Val Trp Glu Ala Leu Val Lys Pro Gly Asp Leu Met Pro Ala Thr Thr 1305 1310 1315			4470
ctg atc cct cca gcc cgc ata gcc gta cct tca cct ctg gat gcc ccg Leu Ile Pro Pro Ala Arg Ile Ala Val Pro Ser Pro Leu Asp Ala Pro 1320 1325 1330			4518
cag ttg ctg cac ttt gtg gac cag tat cga gag cag ctg ata gcc cga Gln Leu Leu His Phe Val Asp Gln Tyr Arg Glu Gln Leu Ile Ala Arg 1335 1340 1345			4566
gtg aca tcg gtg gag gtt gtc ttg gac aaa ctg cat gga cag gtg ctg Val Thr Ser Val Glu Val Val Leu Asp Lys Leu His Gly Gln Val Leu 1350 1355 1360			4614
agc cag gag cag tac gag agg gtg ctg gct gag aac acg agg ccc agc Ser Gln Glu Gln Tyr Glu Arg Val Leu Ala Glu Asn Thr Arg Pro Ser 1365 1370 1375 1380			4662
cag atg cgg aag ctg ttc agc ttg agc cag tcc tgg gac cgg aag tgc Gln Met Arg Lys Leu Phe Ser Leu Ser Gln Ser Trp Asp Arg Lys Cys 1385 1390 1395			4710
aaa gat gga ctc tac caa gcc ctg aag gag acc cat cct cac ctc att Lys Asp Gly Leu Tyr Gln Ala Leu Lys Glu Thr His Pro His Leu Ile 1400 1405 1410			4758
atg gaa ctc tgg gag aag ggc agc aaa aag gga ctc ctg cca ctc agc Met Glu Leu Trp Glu Lys Gly Ser Lys Lys Gly Leu Leu Pro Leu Ser 1415 1420 1425			4806

agc tgaagtatca acaccagccc ttgacccttg agtcctggct ttggctgacc
Ser

4859

cttcttttggg tctcagtttc tttctctgca aacaagttgc catctggttt gccttccagc 4919
actaaagtaa tggaactttg atgatgcctt tgctgggcat tatgtgtcca tgccagggat 4979
gccacagggg gccccagtc aggtggccta acagcatctc agggaaatgtc catctggagc 5039
tggaagacc cctgcagacc tcatagagcc tcatctggtg gccacagcag ccaagcctag 5099
agccctccgg atcccatcca ggcgcaaaga ggaataggag ggacatggaa ccatttgcct 5159
ctggctgtgt cacagggtga gcccctaaat tggggttcag cgtgggaggc cacgtggatt 5219
cttggctttg tacaggaaga tctacaagag caagccaaca gagtaaagtg gaaggaagtt 5279
tattcagaaa ataaaggagt atcacagctc ttttagaatt tgtctagcag gctttccagt 5339
ttttaccaga aaaccctat aaattaaaaa ttttttactt aaatttaaga attaaaaaaa 5399
tacaaaaaag aaaaaatgaa aataaaggaa taagaagtta cctac 5444

<210> 2

<211> 1429

<212> PRT

<213> Homo sapiens

<400> 2

Met	Ala	Gly	Gly	Ala	Trp	Gly	Arg	Leu	Ala	Cys	Tyr	Leu	Glu	Phe	Leu
1			5					10						15	
Lys	Lys	Glu	Glu	Leu	Lys	Glu	Phe	Gln	Leu	Leu	Leu	Ala	Asn	Lys	Ala
		20						25					30		
His	Ser	Arg	Ser	Ser	Ser	Gly	Glu	Thr	Pro	Ala	Gln	Pro	Glu	Lys	Thr
		35						40					45		
Ser	Gly	Met	Glu	Val	Ala	Ser	Tyr	Leu	Val	Ala	Gln	Tyr	Gly	Glu	Gln
	50					55					60				
Arg	Ala	Trp	Asp	Leu	Ala	Leu	His	Thr	Trp	Glu	Gln	Met	Gly	Leu	Arg
65				70						75					80
Ser	Leu	Cys	Ala	Gln	Ala	Gln	Glu	Gly	Ala	Gly	His	Ser	Pro	Ser	Phe
			85						90					95	
Pro	Tyr	Ser	Pro	Ser	Glu	Pro	His	Leu	Gly	Ser	Pro	Ser	Gln	Pro	Thr
			100					105					110		
Ser	Thr	Ala	Val	Leu	Met	Pro	Trp	Ile	His	Glu	Leu	Pro	Ala	Gly	Cys
	115						120						125		
Thr	Gln	Gly	Ser	Glu	Arg	Arg	Val	Leu	Arg	Gln	Leu	Pro	Asp	Thr	Ser
130						135					140				
Gly	Arg	Arg	Trp	Arg	Glu	Ile	Ser	Ala	Ser	Leu	Leu	Tyr	Gln	Ala	Leu
145					150					155					160
Pro	Ser	Ser	Pro	Asp	His	Glu	Ser	Pro	Ser	Gln	Glu	Ser	Pro	Asn	Ala
			165						170					175	
Pro	Thr	Ser	Thr	Ala	Val	Leu	Gly	Ser	Trp	Gly	Ser	Pro	Pro	Gln	Pro
			180					185						190	
Ser	Leu	Ala	Pro	Arg	Glu	Gln	Glu	Ala	Pro	Gly	Thr	Gln	Trp	Pro	Leu
	195							200						205	
Asp	Glu	Thr	Ser	Gly	Ile	Tyr	Tyr	Thr	Glu	Ile	Arg	Glu	Arg	Glu	Arg
210						215					220				
Glu	Lys	Ser	Glu	Lys	Gly	Arg	Pro	Pro	Trp	Ala	Ala	Val	Val	Gly	Thr
225					230					235					240
Pro	Pro	Gln	Ala	His	Thr	Ser	Leu	Gln	Pro	His	His	His	Pro	Trp	Glu
			245						250					255	
Pro	Ser	Val	Arg	Glu	Ser	Leu	Cys	Ser	Thr	Trp	Pro	Trp	Lys	Asn	Glu
			260					265						270	
Asp	Phe	Asn	Gln	Lys	Phe	Thr	Gln	Leu	Leu	Leu	Leu	Gln	Arg	Pro	His

275	280	285
Pro Arg Ser Gln Asp	Pro Leu Val Lys Arg Ser	Trp Pro Asp Tyr Val
290	295	300
Glu Glu Asn Arg Gly His	Leu Ile Glu Ile Arg Asp	Leu Phe Gly Pro
305	310	315
Gly Leu Asp Thr Gln	Glu Pro Arg Ile Val Ile	Leu Gln Gly Ala Ala
325	330	335
Gly Ile Gly Lys Ser Thr	Leu Ala Arg Gln Val Lys	Glu Ala Trp Gly
340	345	350
Arg Gly Gln Leu Tyr Gly	Asp Arg Phe Gln His Val	Phe Tyr Phe Ser
355	360	365
Cys Arg Glu Leu Ala Gln	Ser Lys Val Val Ser	Leu Ala Glu Leu Ile
370	375	380
Gly Lys Asp Gly Thr Ala	Thr Pro Ala Pro Ile Arg	Gln Ile Leu Ser
385	390	395
Arg Pro Glu Arg Leu Leu	Phe Ile Leu Asp Gly Val	Asp Glu Pro Gly
405	410	415
Trp Val Leu Gln Glu Pro	Ser Ser Glu Leu Cys Leu	His Trp Ser Gln
420	425	430
Pro Gln Pro Ala Asp Ala	Leu Leu Gly Ser Leu Leu	Gly Lys Thr Ile
435	440	445
Leu Pro Glu Ala Ser Phe	Leu Ile Thr Ala Arg Thr	Thr Ala Leu Gln
450	455	460
Asn Leu Ile Pro Ser Leu	Glu Gln Ala Arg Trp Val	Glu Val Leu Gly
465	470	475
Phe Ser Glu Ser Ser Arg	Lys Glu Tyr Phe Tyr Arg	Tyr Phe Thr Asp
485	490	495
Glu Arg Gln Ala Ile Arg	Ala Phe Arg Leu Val Lys	Ser Asn Lys Glu
500	505	510
Leu Trp Ala Leu Cys Leu	Val Pro Trp Val Ser Trp	Leu Ala Cys Thr
515	520	525
Cys Leu Met Gln Gln Met	Lys Arg Lys Glu Lys Leu	Thr Leu Thr Ser
530	535	540
Lys Thr Thr Thr Thr Leu	Cys Leu His Tyr Leu Ala	Gln Ala Leu Gln
545	550	555
Ala Gln Pro Leu Gly Pro	Gln Leu Arg Asp Leu Cys	Ser Leu Ala Ala
565	570	575
Glu Gly Ile Trp Gln Lys	Lys Thr Leu Phe Ser Pro	Asp Asp Leu Arg
580	585	590
Lys His Gly Leu Asp Gly	Ala Ile Ile Ser Thr Phe	Leu Lys Met Gly
595	600	605
Ile Leu Gln Glu His Pro	Ile Pro Leu Ser Tyr Ser	Phe Ile His Leu
610	615	620
Cys Phe Gln Glu Phe Phe	Ala Ala Met Ser Tyr Val	Leu Glu Asp Glu
625	630	635
Lys Gly Arg Gly Lys His	Ser Asn Cys Ile Ile Asp	Leu Glu Lys Thr
645	650	655
Leu Glu Ala Tyr Gly Ile	His Gly Leu Phe Gly Ala	Ser Thr Thr Arg
660	665	670
Phe Leu Leu Gly Leu Leu	Ser Asp Glu Gly Glu Arg	Glu Met Glu Asn
675	680	685
Ile Phe His Cys Arg Leu	Ser Gln Gly Arg Asn Leu	Met Gln Trp Val
690	695	700
Pro Ser Leu Gln Leu Leu	Leu Gln Pro His Ser Leu	Glu Ser Leu His
705	710	715
Cys Leu Tyr Glu Thr Arg	Asn Lys Thr Phe Leu Thr	Gln Val Met Ala
725	730	735

His Phe Glu Glu Met Gly Met Cys Val Glu Thr Asp Met Glu Leu Leu
 740 745 750
 Val Cys Thr Phe Cys Ile Lys Phe Ser Arg His Val Lys Lys Leu Gln
 755 760 765
 Leu Ile Glu Gly Arg Gln His Arg Ser Thr Trp Ser Pro Thr Met Val
 770 775 780
 Val Leu Phe Arg Trp Val Pro Val Thr Asp Ala Tyr Trp Gln Ile Leu
 785 790 795 800
 Phe Ser Val Leu Lys Val Thr Arg Asn Leu Lys Glu Leu Asp Leu Ser
 805 810 815
 Gly Asn Ser Leu Ser His Ser Ala Val Lys Ser Leu Cys Lys Thr Leu
 820 825 830
 Arg Arg Pro Arg Cys Leu Leu Glu Thr Leu Arg Leu Ala Gly Cys Gly
 835 840 845
 Leu Thr Ala Glu Asp Cys Lys Asp Leu Ala Phe Gly Leu Arg Ala Asn
 850 855 860
 Gln Thr Leu Thr Glu Leu Asp Leu Ser Phe Asn Val Leu Thr Asp Ala
 865 870 875 880
 Gly Ala Lys His Leu Cys Gln Arg Leu Arg Gln Pro Ser Cys Lys Leu
 885 890 895
 Gln Arg Leu Gln Leu Val Ser Cys Gly Leu Thr Ser Asp Cys Cys Gln
 900 905 910
 Asp Leu Ala Ser Val Leu Ser Ala Ser Pro Ser Leu Lys Glu Leu Asp
 915 920 925
 Leu Gln Gln Asn Asn Leu Asp Asp Val Gly Val Arg Leu Leu Cys Glu
 930 935 940
 Gly Leu Arg His Pro Ala Cys Lys Leu Ile Arg Leu Gly Leu Asp Gln
 945 950 955 960
 Thr Thr Leu Ser Asp Glu Met Arg Gln Glu Leu Arg Ala Leu Glu Gln
 965 970 975
 Glu Lys Pro Gln Leu Leu Ile Phe Ser Arg Arg Lys Pro Ser Val Met
 980 985 990
 Thr Pro Thr Glu Gly Leu Asp Thr Gly Glu Met Ser Asn Ser Thr Ser
 995 1000 1005
 Ser Leu Lys Arg Gln Arg Leu Gly Ser Glu Arg Ala Ala Ser His Val
 1010 1015 1020
 Ala Gln Ala Asn Leu Lys Leu Leu Asp Val Ser Lys Ile Phe Pro Ile
 1025 1030 1035 1040
 Ala Glu Ile Ala Glu Glu Ser Ser Pro Glu Val Val Pro Val Glu Leu
 1045 1050 1055
 Leu Cys Val Pro Ser Pro Ala Ser Gln Gly Asp Leu His Thr Lys Pro
 1060 1065 1070
 Leu Gly Thr Asp Asp Asp Phe Trp Gly Pro Thr Gly Pro Val Ala Thr
 1075 1080 1085
 Glu Val Val Asp Lys Glu Lys Asn Leu Tyr Arg Val His Phe Pro Val
 1090 1095 1100
 Ala Gly Ser Tyr Arg Trp Pro Asn Thr Gly Leu Cys Phe Val Met Arg
 1105 1110 1115 1120
 Glu Ala Val Thr Val Glu Ile Glu Phe Cys Val Trp Asp Gln Phe Leu
 1125 1130 1135
 Gly Glu Ile Asn Pro Gln His Ser Trp Met Val Ala Gly Pro Leu Leu
 1140 1145 1150
 Asp Ile Lys Ala Glu Pro Gly Ala Val Glu Ala Val His Leu Pro His
 1155 1160 1165
 Phe Val Ala Leu Gln Gly Gly His Val Asp Thr Ser Leu Phe Gln Met
 1170 1175 1180
 Ala His Phe Lys Glu Glu Gly Met Leu Leu Glu Lys Pro Ala Arg Val

30	35	40	
ttt gag atc gaa gaa gat tat aaa aat cgt cag ttt ctg ggg cct gaa Phe Glu Ile Glu Glu Asp Tyr Lys Asn Arg Gln Phe Leu Gly Pro Glu 45 50 55 60			493
gga aat gtg gat gtt gag ttg att gat aag agc aca aac aga tac agc Gly Asn Val Asp Val Glu Leu Ile Asp Lys Ser Thr Asn Arg Tyr Ser 65 70 75			541
gtt tgg ttc ccc act gct ggc tgg tat ctg tgg tca gcc aca ggc ctc Val Trp Phe Pro Thr Ala Gly Trp Tyr Leu Trp Ser Ala Thr Gly Leu 80 85 90			589
ggc ttc ctg gta agg gat gag gtc aca gtg acg att gcg ttt ggt tcc Gly Phe Leu Val Arg Asp Glu Val Thr Val Thr Ile Ala Phe Gly Ser 95 100 105			637
tgg agt cag cac ctg gcc ctg gac ctg cag cac cat gaa cag tgg ctg Trp Ser Gln His Leu Ala Leu Asp Leu Gln His His Glu Gln Trp Leu 110 115 120			685
gtg ggc ggc ccc ttg ttt gat gtc act gca gag cca gag gag gct gtc Val Gly Gly Pro Leu Phe Asp Val Thr Ala Glu Pro Glu Glu Ala Val 125 130 135 140			733
gcc gaa atc cac ctc ccc cac ttc atc tcc ctc caa ggt gag gtg gac Ala Glu Ile His Leu Pro His Phe Ile Ser Leu Gln Gly Glu Val Asp 145 150 155			781
gtc tcc tgg ttt ctc gtt gcc cat ttt aag aat gaa ggg atg gtc ctg Val Ser Trp Phe Leu Val Ala His Phe Lys Asn Glu Gly Met Val Leu 160 165 170			829
gag cat cca gcc cgg gtg gag cct ttc tat gct gtc ctg gaa agc ccc Glu His Pro Ala Arg Val Glu Pro Phe Tyr Ala Val Leu Glu Ser Pro 175 180 185			877
agc ttc tct ctg atg ggc atc ctg ctg cgg atc gcc agt ggg act cgc Ser Phe Ser Leu Met Gly Ile Leu Leu Arg Ile Ala Ser Gly Thr Arg 190 195 200			925
ctc tcc atc ccc atc act tcc aac aca ttg atc tat tat cac ccc cac Leu Ser Ile Pro Ile Thr Ser Asn Thr Leu Ile Tyr Tyr His Pro His 205 210 215 220			973
ccc gaa gat att aag ttc cac ttg tac ctt gtc ccc agc gac gcc ttg Pro Glu Asp Ile Lys Phe His Leu Tyr Leu Val Pro Ser Asp Ala Leu 225 230 235			1021
cta aca aag gcg ata gat gat gag gaa gat cgc ttc cat ggt gtg cgc Leu Thr Lys Ala Ile Asp Asp Glu Glu Asp Arg Phe His Gly Val Arg 240 245 250			1069
ctg cag act tcg ccc cca atg gaa ccc ctg aac ttt ggt tcc agt tat Leu Gln Thr Ser Pro Pro Met Glu Pro Leu Asn Phe Gly Ser Ser Tyr 255 260 265			1117

att gtg tct aat tct gct aac ctg aaa gta atg ccc aag gag ttg aaa Ile Val Ser Asn Ser Ala Asn Leu Lys Val Met Pro Lys Glu Leu Lys 270 275 280	1165
ttg tcc tac agg agc cct gga gaa att cag cac ttc tca aaa ttc tat Leu Ser Tyr Arg Ser Pro Gly Glu Ile Gln His Phe Ser Lys Phe Tyr 285 290 295 300	1213
gct ggg cag atg aag gaa ccc att caa ctt gag att act gaa aaa aga Ala Gly Gln Met Lys Glu Pro Ile Gln Leu Glu Ile Thr Glu Lys Arg 305 310 315	1261
cat ggg act ttg gtg tgg gat act gag gtg aag cca gtg gat ctc cag His Gly Thr Leu Val Trp Asp Thr Glu Val Lys Pro Val Asp Leu Gln 320 325 330	1309
ctt gta gct gca tca gcc cct cct cct ttc tca ggt gca gcc ttt gtg Leu Val Ala Ala Ser Ala Pro Pro Pro Phe Ser Gly Ala Ala Phe Val 335 340 345	1357
aag gag aac cac cgg caa ctc caa gcc agg atg ggg gac ctg aaa ggg Lys Glu Asn His Arg Gln Leu Gln Ala Arg Met Gly Asp Leu Lys Gly 350 355 360	1405
gtg ctc gat gat ctc cag gac aat gag gtt ctt act gag aat gag aag Val Leu Asp Asp Leu Gln Asp Asn Glu Val Leu Thr Glu Asn Glu Lys 365 370 375 380	1453
gag ctg gtg gag cag gaa aag aca cgg cag agc aag aat gag gcc ttg Glu Leu Val Glu Gln Glu Lys Thr Arg Gln Ser Lys Asn Glu Ala Leu 385 390 395	1501
ctg agc atg gtg gag aag aaa ggg gac ctg gcc ctg gac gtg ctc ttc Leu Ser Met Val Glu Lys Lys Gly Asp Leu Ala Leu Asp Val Leu Phe 400 405 410	1549
aga agc att agt gaa agg gac cct tac ctc gtg tcc tat ctt aga cag Arg Ser Ile Ser Glu Arg Asp Pro Tyr Leu Val Ser Tyr Leu Arg Gln 415 420 425	1597
cag aat ttg taaaatgagt cagttaggta gtctggaaga gagaatccag Gln Asn Leu 430	1646
cggtctcatt ggaaatggat aaacagaaat gtgatcattg atttcagtgt tcaagacaga	1706
agaagactgg gtaacatcta tcacacaggc tttcaggaca gacttgtaac ctggcatgta	1766
cctattgact gtatcctcat gcattttcct caagaatgtc tgaagaagg agtaatatc	1826
cttttaaaatt ttttccaacc attgcttgat atatactat tttatccatt gacatgattc	1886
ttgaagaccc aggataaagg acatccggat aggtgtgttt atgaaggatg gggcctggaa	1946
aggcaacttt tcttgattaa tgtgaaaaat aattcctatg gacactccgt ttgaagtatc	2006
accttctcat aactaaaagc agaaaagcta acaaaagctt ctgagctgag gacactcaag	2066
gcatacatga tgacagtctt ttttttttt gtatgttagg actttaacac tttatctatg	2126
gctactgtta ttagaacaat gtaaatgtat ttgctgaaag agagcacaaa aatgggagaa	2186
aatgcaaaca tgagcagaaa atattttccc actggtgtgt agcctgctac aaggagttgt	2246
tgggttaaat gttcatggtc aactccaagg aatactgaga tgaaatgtgg taaatcaact	2306
ccacagaacc accaaaaaga aatgaggggt aattcagctt attctgagac agacattcct	2366

ggcaatgtac	catacaaaaa	ataagccaac	tctgacattt	ggattctacc	atagactctg	2426
tcattttgta	gccatttcag	ctgtcttttg	attaatgttt	tcgtggcaca	catatttcca	2486
tccttttatg	tttaatctgt	ttaaaacaag	ttcctagtag	acaccatctg	gttgagtcag	2546
ttttttttat	ggtgtatttt	gaaccatttc	tgatagtctc	ttttaactgg	aagatttcaa	2606
ttacttacgt	taatgtaatt	attaatatgt	taggatttat	cctcagtcag	ccagtttggt	2666
atgtcttttc	tattctactg	ttatcacatt	tgtaccactt	aaagtggaa	ctaggcactt	2726
tatcaccatt	tagatcctat	taccttttct	catctaggat	atagttatct	tctacataat	2786
ctttctgtat	cttaaaaccc	atcaataaat	tattatatat	tttctacttt	taatcactca	2846
gaagatttaa	aaaactcatg	agaagagtaa	tctgttatgt	ttttccagat	atttaccatt	2906
tctgttgctc	ttccttcatt	attttccaaa	tttcgttctg	caaatttcca	cttcttctga	2966
tagacgtttt	ttagtctttt	tagagtgggt	ctgataggta	cagattctct	tattttttgc	3026
ttcctctgag	gacatctttt	tctcaccttc	attctcagtg	atgttttttg	cttgtagtat	3086
ttttagttga	cattgttttt	tgttcagcag	tttcctttta	gcttcogtat	ttcctgatga	3146
gaaatctgca	gtcattcaaa	ttgttgtttc	cctgtatgta	gtgtgtcatt	tttctgtcag	3206
atttcaagggt	atttatcttt	agtttttagc	catttcatta	tggtggggat	gagtttccct	3266
gttttattcc	ctttggaatt	tgctccaatt	cataaatttg	cagttttatg	tcttttacca	3326
aacttagagg	ttttcagcct	aattttctaaa	aatacttttt	attagcctga	ttttcatctt	3386
tataggaaat	agttaaagtg	atgacaagtt	ccaatagctt	atatgccag	aaggccttca	3446
aaataagaat	tttgaaagaa	tacagaaaac	aaacttttat	atccttctca	tgtcttctac	3506
tgtaaaattc	atatgctttg	ctactctaaa	cctagtttga	aatcaacagt	cttgagaata	3566
gatgaaaatt	ttgatgaata	gtggaattct	tttaaatgga	aacctcttac	atgtgatttt	3626
ccttgccatc	tagaaataaa	ccatagtatt	tatgttgaat	caatcaatat	tatattttgt	3686
ttttttcctc	ctcttctgag	actcttattg	tggaaatgtt	agacttttat	gttttcctaa	3746
atgtccctga	tattctactt	atttagaaca	tcttttcatt	ttttccatta	ttctgattgg	3806
gtaattttta	tttgtctatt	ttcaaatttg	ctggagtggt	cacctgttgt	tgtctgtgtc	3866
gtcccactga	gtgcattcac	caccttttaa	attttggtca	ctgtatgtat	cagttctaaa	3926
atttccattt	tgttctctat	attttaaaatt	tcttggttta	tattctattt	tcctgcaaatt	3986
gtgtcagcat	ttgcttggtt	gagctttttt	tttttcaaga	cagggtctca	actctgttac	4046
ccaggctgga	gtgcagtggt	gcgatctcag	ctcactgcaa	cctctgcctc	ctgggtcaag	4106
cgattattgt	gcctcagcct	cctgagtagc	tgggattaca	ggcatgcacc	accacagccc	4166
agctaatttt	ttgtattttt	agtagagaca	gagttttgct	atgttgcca	ggctgggttt	4226
gaactcctgg	cctcaagtga	tccaccacc	tcagcctccc	aaagtgctgg	gattacaggc	4286
cactacacct	ggcacatttg	agtatttttt	tttttttttt	ttttttgaga	tggagtctcg	4346
ctctgtcatc	taggctggag	tgcatgtgtg	tgatctcagc	tcactgcagc	ctctgtctcc	4406
cgggctcaag	cgattctctt	gcctcagcct	cctgagtagc	taggactaca	ggtgcatgcc	4466
aacacgccc	gctaattttt	ttaaaaaata	tttttagtag	agacagggtt	tcaccatttt	4526
ggccaggatg	gtctcgatct	cctgacctca	tgatccaccc	gcctcgccct	tccaaagtgc	4586
tgggattaca	ggcatgagcc	accgtgcctg	gcctcatttg	agtattttta	taatgtctct	4646
tttaaagtct	ttgtcagata	attccactgt	acatgttatt	cagtgttttg	tgtccactga	4706
gttgtcattt	gccagacaag	tggagatttt	tgcagctcat	ccttgatttc	tcagtagttc	4766
cgatatgtac	cctcgacatg	tgaatgttat	cttatgagac	tctgttttat	ttgtatccaa	4826
cagaagatgt	ttattattta	tttggttttc	tgtgaactga	ggtcttaata	tcagctcatt	4886
ttaaaagtct	ttgcagtggt	attcggatct	atcctgtgtg	tgccatagag	attgggtgca	4946
gtgtatcctg	ttagctccat	tctcagggcg	tttgaatgtg	aattaggacc	agcgcaatga	5006
atgctcaagt	tgggggttggg	cgttagaatt	cataaaagtc	tttatatgct	cag	5059

<210> 4

<211> 431

<212> PRT

<213> Homo sapiens

<400> 4

Met	Met	Arg	Gln	Arg	Gln	Ser	His	Tyr	Cys	Ser	Val	Leu	Phe	Leu	Ser
1			5					10						15	
Val	Asn	Tyr	Leu	Gly	Gly	Thr	Phe	Pro	Gly	Asp	Ile	Cys	Ser	Glu	Glu
			20					25					30		
Asn	Gln	Ile	Val	Ser	Ser	Tyr	Ala	Ser	Lys	Val	Cys	Phe	Glu	Ile	Glu

35	40	45
Glu Asp Tyr Lys Asn Arg Gln Phe Leu Gly Pro	Glu Gly Asn Val Asp	
50	55	60
Val Glu Leu Ile Asp Lys Ser Thr Asn Arg Tyr Ser Val Trp Phe Pro		
65	70	75
Thr Ala Gly Trp Tyr Leu Trp Ser Ala Thr Gly Leu Gly Phe Leu Val		
	85	90
Arg Asp Glu Val Thr Val Thr Ile Ala Phe Gly Ser Trp Ser Gln His		
	100	105
Leu Ala Leu Asp Leu Gln His His Glu Gln Trp Leu Val Gly Gly Pro		
	115	120
Leu Phe Asp Val Thr Ala Glu Pro Glu Glu Ala Val Ala Glu Ile His		
	130	135
Leu Pro His Phe Ile Ser Leu Gln Gly Glu Val Asp Val Ser Trp Phe		
145	150	155
Leu Val Ala His Phe Lys Asn Glu Gly Met Val Leu Glu His Pro Ala		
	165	170
Arg Val Glu Pro Phe Tyr Ala Val Leu Glu Ser Pro Ser Phe Ser Leu		
	180	185
Met Gly Ile Leu Leu Arg Ile Ala Ser Gly Thr Arg Leu Ser Ile Pro		
	195	200
Ile Thr Ser Asn Thr Leu Ile Tyr Tyr His Pro His Pro Glu Asp Ile		
	210	215
Lys Phe His Leu Tyr Leu Val Pro Ser Asp Ala Leu Leu Thr Lys Ala		
225	230	235
Ile Asp Asp Glu Glu Asp Arg Phe His Gly Val Arg Leu Gln Thr Ser		
	245	250
Pro Pro Met Glu Pro Leu Asn Phe Gly Ser Ser Tyr Ile Val Ser Asn		
	260	265
Ser Ala Asn Leu Lys Val Met Pro Lys Glu Leu Lys Leu Ser Tyr Arg		
	275	280
Ser Pro Gly Glu Ile Gln His Phe Ser Lys Phe Tyr Ala Gly Gln Met		
	290	295
Lys Glu Pro Ile Gln Leu Glu Ile Thr Glu Lys Arg His Gly Thr Leu		
305	310	315
Val Trp Asp Thr Glu Val Lys Pro Val Asp Leu Gln Leu Val Ala Ala		
	325	330
Ser Ala Pro Pro Pro Phe Ser Gly Ala Ala Phe Val Lys Glu Asn His		
	340	345
Arg Gln Leu Gln Ala Arg Met Gly Asp Leu Lys Gly Val Leu Asp Asp		
	355	360
Leu Gln Asp Asn Glu Val Leu Thr Glu Asn Glu Lys Glu Leu Val Glu		
	370	375
Gln Glu Lys Thr Arg Gln Ser Lys Asn Glu Ala Leu Leu Ser Met Val		
385	390	395
Glu Lys Lys Gly Asp Leu Ala Leu Asp Val Leu Phe Arg Ser Ile Ser		
	405	410
Glu Arg Asp Pro Tyr Leu Val Ser Tyr Leu Arg Gln Gln Asn Leu		
	420	425
		430

<210> 5

<211> 4287

<212> DNA

<213> Homo sapiens

<400> 5

atggctggcg gagcctgggg ccgcctggcc tggttacttgg agttcctgaa gaaggaggag

ctgaaggagt	tccagcttct	gctcgccaat	aaagcgact	ccaggagctc	ttcgggtgag	120
acaccgcctc	agccagagaa	gacgagtggc	atggaggtgg	cctcgtacct	ggtggctcag	180
tatggggagc	agcgggcctg	ggacctagcc	ctccatacct	gggagcagat	ggggctgagg	240
tcactgtgcg	cccaagccca	ggaaggggca	ggccactctc	cctcattccc	ctacagccca	300
agtgaacccc	acctgggggtc	tcccagccaa	cccacctcca	ccgcagtgtc	aatgccttgg	360
atccatgaat	tgcgggcggg	gtgcacccag	ggctcagaga	gaagggtttt	gagacagctg	420
cctgacacat	ctggagcgcg	ctggagagaa	atctctgcct	cactcctcta	ccaagctctt	480
ccaagctccc	cagaccatga	gtctccaagc	caggagtcaac	ccaacgcccc	cacatccaca	540
gcagtgtctg	ggagctgggg	atccccacct	cagcccagcc	tagcacccag	agagcaggag	600
gctcctggga	cccaatggcc	tctggatgaa	acgtcaggaa	tttactacac	agaaatcaga	660
gaaagagaga	gagagaaatc	agagaaaagg	aggcccccat	gggcagcggg	ggtaggaacg	720
ccccacagg	cgacaccag	cctacagccc	caccaccacc	catgggagcc	ttctgtgaga	780
gagagcctct	gttccacatg	gccctggaaa	aatgaggatt	ttaacaaaaa	attcacacag	840
ctgtacttct	tacaaagacc	tcaccccaga	agccaagatc	ccctggtcaa	gagaagctgg	900
cctgattatg	tggaggagaa	tcgaggacat	ttaattgaga	tcagagactt	atttggccca	960
ggcctggata	cccaagaacc	tcgcatagtc	atactgcagg	gggctgctgg	aattgggaag	1020
tcaacactgg	ccaggcaggt	gaaggaagcc	tgggggagag	gccagctgta	tggggaccgc	1080
ttccagcatg	tcttctactt	cagctgcaga	gagctggccc	agtccaaggt	ggtgagtctc	1140
gctgagctca	tcggaaaaga	tgggacagcc	actccggctc	ccattagaca	gacccgtgtc	1200
aggccagagc	ggctgtctct	catcctcgat	ggtgtagatg	agccaggatg	ggtcttgacg	1260
gagccgagtt	ctgagctctg	tctgcactgg	agccagccac	agccggcgga	tgcactgctg	1320
ggcagtttgc	tggggaaaac	tatacttccc	gaggcatcct	tcctgatcac	ggctcggacc	1380
acagctctgc	agaacctcat	tccttctttg	gagcaggcac	gttgggtaga	ggtcctgggg	1440
ttctctgagt	ccagcaggaa	ggaatatatt	tacagatatt	tcacagatga	aaggcaagca	1500
attagagcct	ttaggttggt	caaatacaac	aaagagctct	gggccctgtg	tcttgtgccc	1560
tgggtgtcct	ggctggcctg	cacttgcttg	atgcagcaga	tgaagcggaa	ggaaaaactc	1620
acactgactt	ccaagaccac	cacaaccctc	tgtctacatt	accttgccca	ggctctccaa	1680
gctcagccat	tgggacccca	gctcagagac	ctctgtctct	tggctgctga	gggcatctgg	1740
caaaaaaaga	cccttttcag	tccagatgac	ctcaggaagc	atgggttaga	tggggccatc	1800
atctccacct	tcttgaagat	gggtattctt	caagagcacc	ccatccctct	gagctacagc	1860
ttcattcacc	tctgtttcca	agagtctctt	gcagcaatgt	cctatgtctt	ggaggatgag	1920
aaggggagag	gtaaacattc	taattgcatc	atagatttgg	aaaagacgct	agaagcatat	1980
ggaatacatg	gcctgtttgg	ggcatcaacc	acacgtttcc	tattgggcct	gttaagtgat	2040
gagggggaga	gagagatgga	gaacatcttt	cactgccggc	tgtctcaggg	gaggaacctg	2100
atgcagtggg	tcccgctcct	gcagctgctg	ctgcagccac	actctctgga	gtccctccac	2160
tgcttgtagc	agactcgga	caaaacgttc	ctgacacaag	tgatggccca	tttcaagaa	2220
atgggcatgt	gtgtagaaac	agacatggag	ctcttagtgt	gcactttctg	cattaaattc	2280
agccgccacg	tgaagaagct	tcagctgatt	gagggcaggc	agcacagatc	aacatggagc	2340
cccaccatgg	tagtctgttt	cagggtgggtc	ccagtcacag	atgcctattg	gcagattctc	2400
ttctccgtcc	tcaaggtcac	cagaaacctg	aaggagctgg	acctaagtgg	aaactcgctg	2460
agccactctg	cagtgaagag	tctttgtaag	accctgagac	gccctcgctg	cctcctggag	2520
accctgcggg	tggctggctg	tggcctcaca	gctgaggact	gcaaggacct	tgcctttggg	2580
ctgagagcca	accagaccct	gaccgagctg	gacctgagct	tcaatgtgct	cacggatgct	2640
ggagccaaac	acctttgcca	gagactgaga	cagccgagct	gcaagctaca	gcgactgcag	2700
ctggtcagct	gtggcctcac	gtctgactgc	tgccaggacc	tggcctctgt	gcttagtgcc	2760
agccccagcc	tgaaggagct	agacctgcag	cagaacaacc	tggatgacgt	tggcgtgcga	2820
ctgctctgtg	aggggctcag	gcatacctgcc	tgcaaaactca	tacgcctggg	gctggaccag	2880
acaactctga	gtgatgagat	gaggcaggaa	ctgaggggccc	tggagcagga	gaaacctcag	2940
ctgctcatct	tcagcagacg	gaaaccaagt	gtgatgaccc	ctactgaggg	cctggatacg	3000
ggagagatga	gtaaatgac	atcctcactc	aagcggcaga	gactcggatc	agagagggcg	3060
gcttcccatg	ttgtcagggc	taatctcaaa	ctcctggacg	tgagcaagat	cttcccaatt	3120
gctgagattg	cagaggaaaag	ctccccagag	gtagtaccgg	tggaaactct	gtgcgtgcct	3180
tctcctgcct	ctcaagggga	cctgcatacg	aagcctttgg	ggactgacga	tgacttctgg	3240
ggccccacgg	ggcctgtggc	tactgaggta	gttgacaaaag	aaaagaactt	gtaccgagtt	3300
cacttccctg	tagctggctc	ctaccgctgg	cccaacacgg	gtctctgctt	tgtgatgaga	3360
gaagcgggtga	ccgttgagat	tgaattctgt	gtgtgggacc	agttcctggg	tgagatcaac	3420
ccacagcaca	gctggatggg	ggcagggcct	ctgctggaca	tcaaggctga	gcctggagct	3480

gtggaagctg	tgcacctccc	tcactttgtg	gctctccaag	ggggccatgt	ggacacatcc	3540
ctgttccaaa	tggcccactt	taaagaggag	gggatgctcc	tggagaagcc	agccagggtg	3600
gagctgcac	acatagttct	ggaaaacccc	agcttctccc	ccttgggagt	cctcctgaaa	3660
atgatccata	atgccctgcg	cttcattccc	gtcacctctg	tgggtgttgc	ttaccaccgc	3720
gtccatcctg	aggaagtcac	cttcacctc	tacctgatcc	caagtgactg	ctccattcgg	3780
aaggaactgg	agctctgcta	tcgaagccct	ggagaagacc	agctgttctc	ggagttctac	3840
gttggccact	tgggatcagg	gatcaggctg	caagtgaagc	acaagaaaga	tgagactctg	3900
gtgtgggagg	ccttggtgaa	accaggagat	ctcatgcctg	caactactct	gatccctcca	3960
gcccccatag	ccgtaccttc	acctctggat	gccccgcagt	tgctgcactt	tgtggaccag	4020
tatcgagagc	agctgatagc	ccgagtgcac	tcgggtggagg	ttgtcttggg	caaactgcac	4080
ggacaggtgc	tgagccagga	gcagtacgag	aggggtgctgg	ctgagaacac	gaggcccagc	4140
cagatgcgga	agctgttcag	cttgagccag	tcctgggacc	ggaagtgcac	agatggactc	4200
taccaagccc	tgaaggagac	ccatcctcac	ctcattatgg	aactctggga	gaagggcagc	4260
aaaaagggac	tcctgccact	cagcagc				4287

<210> 6

<211> 1293

<212> DNA

<213> Homo sapiens

<400> 6

atgatgagac	agaggcagag	ccattattgt	tccgtgctgt	tcctgagtgt	caactatctg	60
ggggggacat	tcccaggaga	catttgcctc	gaagagaatc	aaatagtttc	ctcttatgct	120
tctaaagtct	gttttgagat	cgaagaagat	tataaaaatc	gtcagtttct	ggggcctgaa	180
ggaaatgtgg	atgttgagtt	gattgataag	agcacaaaca	gatacagcgt	ttgggtcccc	240
actgctggct	ggtatctgtg	gtcagccaca	ggcctcggct	tcctggtaag	ggatgaggtc	300
acagtgcga	ttgcgttttg	ttcctggagt	cagcacctgg	ccctggacct	gcagcaccat	360
gaacagtggc	tggtgggcgg	ccccttgttt	gatgtcactg	cagagccaga	ggaggtgtc	420
gccgaaatcc	acctccccc	cttcactctc	ctccaagggtg	aggtggacgt	ctcctggttt	480
ctcgttgccc	attttaagaa	tgaagggatg	gtcctggagc	atccagcccg	ggtggagcct	540
ttctatgctg	tcctggaaaag	ccccagcttc	tctctgatgg	gcacccctgt	gcggatcgcc	600
agtgggactc	gcctctccat	ccccatcact	tccaacacat	tgatctatta	tcacccccac	660
cccgaagata	ttaagttcca	cttgtaacct	gtccccagcg	acgccttgct	aacaaaggcg	720
atagatgatg	aggaagatcg	cttccatggt	gtgcgcctgc	agacttcgcc	cccaatggaa	780
ccctgaact	ttggttccag	ttatattgtg	tctaattctg	ctaacctgaa	agtaatgccc	840
aaggagtga	aattgtccta	caggagccct	ggagaaattc	agcacttctc	aaaattctat	900
gctgggcaga	tgaaggaaac	cattcaactt	gagattactg	aaaaaagaca	tgggactttg	960
gtgtgggata	ctgaggtgaa	gccagtggat	ctccagcttg	tagctgcac	agccccctct	1020
cctttctcag	gtgcagcctt	tgtgaaggag	aaccaccggc	aactccaagc	caggatgggg	1080
gacctgaaag	gggtgctcga	tgatctccag	gacaatgagg	ttcttactga	gaatgagaag	1140
gagctggtgg	agcaggaaaa	gacacggcag	agcaagaatg	aggccttgct	gagcatggtg	1200
gagaagaaag	gggacctggc	cctggacgtg	ctcttcagaa	gcattagtga	aagggaccct	1260
tacctcgtgt	cctatcttag	acagcagaat	ttg			1293

<210> 7

<211> 90

<212> PRT

<213> Homo sapiens

<400> 7

Ser	Ala	Ala	Lys	Pro	Gly	Leu	His	Phe	Ile	Asp	Gln	His	Arg	Ala	Ala
1			5						10					15	
Leu	Ile	Ala	Arg	Val	Thr	Asn	Val	Glu	Trp	Leu	Leu	Asp	Ala	Leu	Tyr
			20					25					30		
Gly	Lys	Val	Leu	Thr	Asp	Glu	Gln	Tyr	Gln	Ala	Val	Arg	Ala	Glu	Pro
			35					40					45		
Thr	Asn	Pro	Ser	Lys	Met	Arg	Lys	Leu	Phe	Ser	Phe	Thr	Pro	Ala	Trp

50		55		60
Asn Trp Thr Cys Lys Asp Leu Leu Leu Gln Ala Leu Arg Glu Ser Gln				
65		70		75
Ser Tyr Leu Val Glu Asp Leu Glu Arg Ser				80
	85		90	

<210> 8
 <211> 89
 <212> PRT
 <213> Homo sapiens

<400> 8

Met Asp Ala Lys Ala Arg Asn Cys Leu Leu Gln His Arg Glu Ala Leu				
1	5	10	15	
Glu Lys Asp Ile Lys Thr Ser Tyr Ile Met Asp His Met Ile Ser Asp				
	20	25	30	
Gly Phe Leu Thr Ile Ser Glu Glu Glu Lys Val Arg Asn Glu Pro Thr				
	35	40	45	
Gln Gln Gln Arg Ala Ala Met Leu Ile Lys Met Ile Leu Lys Lys Asp				
	50	55	60	
Asn Asp Ser Tyr Val Ser Phe Tyr Asn Ala Leu Leu His Glu Gly Tyr				
65	70	75	80	
Lys Asp Leu Ala Ala Leu Leu His Asp				
	85			

<210> 9
 <211> 92
 <212> PRT
 <213> Homo sapiens

<400> 9

Glu Ser His Pro His Ile Gln Leu Leu Lys Ser Asn Arg Glu Leu Leu				
1	5	10	15	
Val Thr His Ile Arg Asn Thr Gln Cys Leu Val Asp Asn Leu Leu Lys				
	20	25	30	
Asn Asp Tyr Phe Ser Ala Glu Asp Ala Glu Ile Val Cys Ala Cys Pro				
	35	40	45	
Thr Gln Pro Asp Lys Val Arg Lys Ile Leu Asp Leu Val Gln Ser Lys				
	50	55	60	
Gly Glu Glu Val Ser Glu Phe Phe Leu Tyr Leu Leu Gln Gln Leu Ala				
65	70	75	80	
Asp Ala Tyr Val Asp Leu Arg Pro Trp Leu Leu Glu				
	85	90		

<210> 10
 <211> 89
 <212> PRT
 <213> Homo sapiens

<400> 10

Met Ala Asp Lys Val Leu Lys Glu Lys Arg Lys Leu Phe Ile Arg Ser				
1	5	10	15	
Met Gly Glu Gly Thr Ile Asn Gly Leu Leu Asp Glu Leu Leu Gln Thr				
	20	25	30	
Arg Val Leu Asn Lys Glu Glu Met Glu Lys Val Lys Arg Glu Asn Ala				
	35	40	45	
Thr Val Met Asp Lys Thr Arg Ala Leu Ile Asp Ser Val Ile Pro Lys				

50		55		60											
Gly	Ala	Gln	Ala	Cys	Gln	Ile	Cys	Ile	Thr	Tyr	Ile	Cys	Glu	Glu	Asp
65					70					75					80
Ser	Tyr	Leu	Ala	Gly	Thr	Leu	Gly	Leu							
				85											

<210> 11
 <211> 89
 <212> PRT
 <213> Homo sapiens

<400> 11
Ile Ala Gln Gln Trp Ile Gln Ser Lys Arg Glu Asp Ile Val Asn Gln
1 5 10 15
Met Thr Glu Ala Cys Leu Asn Gln Ser Leu Asp Ala Leu Leu Ser Arg
20 25 30
Asp Leu Ile Met Lys Glu Asp Tyr Glu Leu Val Ser Thr Lys Pro Thr
35 40 45
Arg Thr Ser Lys Val Arg Gln Leu Leu Asp Thr Thr Asp Ile Gln Gly
50 55 60
Glu Glu Phe Ala Lys Val Ile Val Gln Lys Leu Lys Asp Asn Lys Gln
65 70 75 80
Met Gly Leu Gln Pro Tyr Pro Glu Ile
85